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OPIPE

RAW SEQUENCE LISTING DATE: 08/29/2002
PATENT APPLICATION: US/09/909,566C TIME: 13:41:29

Input Set : A:\BB1465 US NA substitute seq lst..txt
Output Set: N:\CRF3\08292002\I909566C.raw

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54 gattggatg gataataata aattgaaatg ttttctttt caaatccgaa aaa 1733
 57 <210> SEQ ID NO: 2
 58 <211> LENGTH: 500
 59 <212> TYPE: PRT
 60 <213> ORGANISM: Euphorbia lagascae
 62 <400> SEQUENCE: 2
 63 Met Glu Gln Lys Asn Leu Ser Phe Pro Ser Ile Leu Ile Ser Phe Leu
 64 1 5 10 15
 66 Leu Val Leu Ile Leu Val Val Val Met Arg Leu Trp Lys Lys Gln Asn
 67 20 25 30
 69 Pro Pro Pro Gly Pro Trp Lys Phe Pro Ile Ile Gly Asn Leu Pro His
 70 35 40 45
 72 Leu Leu Leu Thr Ser Asp Leu Gly His Glu Arg Phe Arg Ala Leu Ala
 73 50 55 60
 75 Gln Ile Tyr Gly Pro Val Met Ser Leu Gln Ile Gly Gln Val Ser Ala
 76 65 70 75 80
 78 Val Val Ile Ser Ser Ala Glu Ala Ala Lys Glu Val Met Lys Thr Gln
 79 85 90 95
 81 Ala Asp Ala Phe Ala Gln Arg Pro Ile Val Leu Asp Ala Gln Ile Val
 82 100 105 110
 84 Phe Tyr Asn Arg Lys Asp Val Leu Phe Ala Ser Tyr Gly Asp His Trp
 85 115 120 125
 87 Arg Gln Met Lys Lys Ile Trp Ile Leu Glu Phe Leu Ser Ala Lys Lys
 88 130 135 140
 90 Val Gln Ser Ser Arg Leu Ile Arg Glu Glu Glu Met Glu Asp Ala Ile
 91 145 150 155 160
 93 Thr Phe Leu Arg Ser Lys Ala Gly Ser Pro Val Asn Ile Thr Lys Ile
 94 165 170 175
 96 Ile Tyr Gly Ile Ile Ser Ile Met Ile Arg Thr Ser Val Gly Asn
 97 180 185 190
 99 Cys Lys Gln Lys Glu Arg Leu Leu Ser Val Ala Asp Ala Val Asn Glu
 100 195 200 205
 102 Ala Ala Thr Ser Phe Gly Thr Ala Asp Ala Phe Pro Thr Trp Lys Leu
 103 210 215 220
 105 Leu His Tyr Ile Ile Gly Ala Glu Ser Lys Pro Arg Arg Leu His Gln
 106 225 230 235 240
 108 Glu Ile Asp Asp Ile Leu Glu Glu Ile Leu Asn Glu His Lys Ala Asn
 109 245 250 255
 111 Lys Pro Phe Glu Ala Asp Asn Leu Met Asp Val Leu Leu Asn Leu Gln
 112 260 265 270
 114 Lys Asn Gly Asn Val Pro Val Pro Val Thr Asn Glu Ser Ile Lys Ala
 115 275 280 285
 117 Ser Val Leu Gln Met Phe Thr Ala Gly Ser Glu Thr Thr Ser Lys Ala
 118 290 295 300
 120 Thr Glu Trp Val Met Ala Glu Leu Met Lys Asn Pro Thr Glu Leu Arg
 121 305 310 315 320
 123 Lys Ala Gln Glu Glu Val Arg Gln Val Phe Gly Glu Met Gly Lys Val
 124 325 330 335
 126 Asp Glu Ser Arg Phe His Asp Leu Lys Phe Phe Lys Leu Val Val Lys

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127 340 345 350
 129 Glu Thr Leu Arg Leu His Pro Pro Val Val Leu Ile Pro Arg Glu Cys
 130 355 360 365
 132 Arg Glu Thr Thr Arg Ile Asp Gly Tyr Glu Ile His Pro Asn Thr Arg
 133 370 375 380
 135 Ile Val Val Asn Ala Trp Ala Ile Gly Arg Asp Pro Asn Thr Trp Ser
 136 385 390 395 400
 138 Glu Pro Gly Lys Phe Asn Pro Glu Arg Phe Lys Asp Cys Ala Ile Asp
 139 405 410 415
 141 Tyr Lys Gly Thr Thr Phe Glu Leu Val Pro Phe Gly Ala Gly Lys Arg
 142 420 425 430
 144 Ile Cys Pro Gly Ile Thr Ser Ala Ile Thr Asn Leu Glu Tyr Val Ile
 145 435 440 445
 147 Ile Asn Leu Leu Tyr His Phe Asn Trp Glu Leu Ala Asp Gly Ile Thr
 148 450 455 460
 150 Pro Gln Thr Leu Asp Met Thr Glu Ala Ile Gly Gly Ala Leu Arg Lys
 151 465 470 475 480
 153 Lys Ile Asp Leu Lys Leu Ile Pro Ile Pro Tyr Gln Val Ser Leu Gly
 154 485 490 495
 156 Ser Asn Ile Ser
 157 500
 160 <210> SEQ ID NO: 3
 161 <211> LENGTH: 502
 162 <212> TYPE: PRT
 163 <213> ORGANISM: Capsicum annuum
 165 <400> SEQUENCE: 3
 166 Met Glu Ile Gln Phe Thr Asn Leu Val Ala Phe Leu Leu Phe Leu Ser
 167 1 5 10 15
 169 Ser Ile Ile Leu Leu Lys Lys Trp Lys Thr Gln Lys Leu Asn Leu
 170 20 25 30
 172 Pro Pro Gly Pro Trp Lys Leu Pro Phe Ile Gly Ser Leu His His Leu
 173 35 40 45
 175 Ala Val Ala Gly Pro Leu Pro His His Gly Leu Lys Asn Leu Ala Lys
 176 50 55 60
 178 Leu Tyr Gly Pro Leu Met His Leu Arg Leu Gly Glu Ile Pro Thr Val
 179 65 70 75 80
 181 Ile Ile Ser Ser Pro Arg Met Ala Lys Glu Val Leu Lys Thr His Asp
 182 85 90 95
 184 Leu Ala Phe Ala Thr Arg Pro Lys Leu Val Val Ala Asp Ile Val His
 185 100 105 110
 187 Tyr Asp Ser Thr Asp Ile Ala Phe Ser Pro Tyr Gly Glu Tyr Trp Arg
 188 115 120 125
 190 Gln Ile Arg Lys Ile Cys Ile Leu Glu Leu Leu Ser Ala Lys Met Val
 191 130 135 140
 193 Lys Phe Phe Ser Ser Ile Arg Gln Asp Glu Leu Ser Met Met Val Ser
 194 145 150 155 160
 196 Ser Ile Arg Thr Met Pro Asn Phe Pro Val Asn Leu Thr Asp Lys Ile
 197 165 170 175
 199 Phe Trp Phe Thr Ser Ser Val Thr Cys Arg Ser Ala Leu Gly Lys Ile

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200 180 185 190
 202 Cys Arg Asp Gln Asp Lys Leu Ile Phe Met Arg Glu Ile Ile Ser
 203 195 200 205
 205 Leu Thr Gly Gly Phe Ser Ile Ala Asp Phe Phe Pro Thr Trp Lys Met
 206 210 215 220
 208 Leu His Asp Val Gly Gly Ser Lys Thr Arg Leu Leu Lys Ala His Arg
 209 225 230 235 240
 211 Lys Ile Asp Glu Ile Leu Glu His Val Val Asn Glu His Lys Gln Asn
 212 245 250 255
 214 Arg Ala Asp Gly Gln Lys Gly Asn Gly Glu Phe Gly Gly Glu Asp Leu
 215 260 265 270
 217 Ile Asp Val Leu Leu Arg Val Arg Glu Ser Gly Glu Val Gln Ile Ser
 218 275 280 285
 220 Ile Thr Asp Asp Asn Ile Lys Ser Ile Leu Val Asp Met Phe Ser Ala
 221 290 295 300
 223 Gly Ser Glu Thr Ser Ser Thr Thr Ile Ile Trp Ala Leu Ala Glu Met
 224 305 310 315 320
 226 Met Lys Lys Pro Ser Val Leu Ala Lys Ala Gln Ala Glu Val Arg Gln
 227 325 330 335
 229 Val Leu Lys Glu Lys Lys Gly Phe Gln Gln Ile Asp Leu Asp Glu Leu
 230 340 345 350
 232 Lys Tyr Leu Lys Leu Val Ile Lys Glu Thr Leu Arg Met His Pro Pro
 233 355 360 365
 235 Ile Pro Leu Leu Val Pro Arg Glu Cys Met Lys Asp Thr Lys Ile Asp
 236 370 375 380
 238 Gly Tyr Asn Ile Pro Phe Lys Thr Arg Val Ile Val Asn Ala Trp Ala
 239 385 390 395 400
 241 Ile Gly Arg Asp Pro Glu Ser Trp Asp Asp Pro Glu Ser Phe Ser Pro
 242 405 410 415
 244 Glu Arg Phe Glu Asn Ser Ser Val Asp Phe Leu Gly Ser His His Gln
 245 420 425 430
 247 Phe Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Pro Gly Met Leu Phe
 248 435 440 445
 250 Gly Leu Ala Asn Val Gly Gln Pro Leu Ala Gln Leu Tyr His Phe
 251 450 455 460
 253 Asp Arg Lys Leu Pro Asn Gly Gln Ser His Glu Asn Leu Asp Met Thr
 254 465 470 475 480
 256 Glu Ser Pro Gly Ile Ser Ala Thr Arg Lys Asp Asp Leu Val Leu Ile
 257 485 490 495
 259 Ala Thr Pro Tyr Asp Pro
 260 500
 263 <210> SEQ ID NO: 4
 264 <211> LENGTH: 51
 265 <212> TYPE: DNA
 266 <213> ORGANISM: artificial sequence
 268 <220> FEATURE:
 269 <221> NAME/KEY: misc_feature
 270 <222> LOCATION:
 271 <223> OTHER INFORMATION: oligonucleotide primer

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273 <400> SEQUENCE: 4
274 tcaaggagaaa aaaaccccg atccatggag cagaaaaatc tctctttcc g 51
277 <210> SEQ ID NO: 5
278 <211> LENGTH: 35
279 <212> TYPE: DNA
280 <213> ORGANISM: artificial sequence
282 <220> FEATURE:
283 <221> NAME/KEY: misc_feature
284 <222> LOCATION:
285 <223> OTHER INFORMATION: oligonucleotide primer
287 <400> SEQUENCE: 5
288 ggccagtgaa ttgttaatacg actcactata gggcg 35
291 <210> SEQ ID NO: 6
292 <211> LENGTH: 35
293 <212> TYPE: DNA
294 <213> ORGANISM: artificial sequence
296 <220> FEATURE:
297 <221> NAME/KEY: misc_feature
298 <222> LOCATION:
299 <223> OTHER INFORMATION: oligonucleotide primer
301 <400> SEQUENCE: 6
302 gcggccgcga attcgaaaaa tggagcagaa aaatc 35
305 <210> SEQ ID NO: 7
306 <211> LENGTH: 35
307 <212> TYPE: DNA
308 <213> ORGANISM: artificial sequence
310 <220> FEATURE:
311 <221> NAME/KEY: misc_feature
312 <222> LOCATION:
313 <223> OTHER INFORMATION: oligonucleotide primer
315 <400> SEQUENCE: 7
316 gcggccgcgg atccttagaa catcgtaat taaag 35

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